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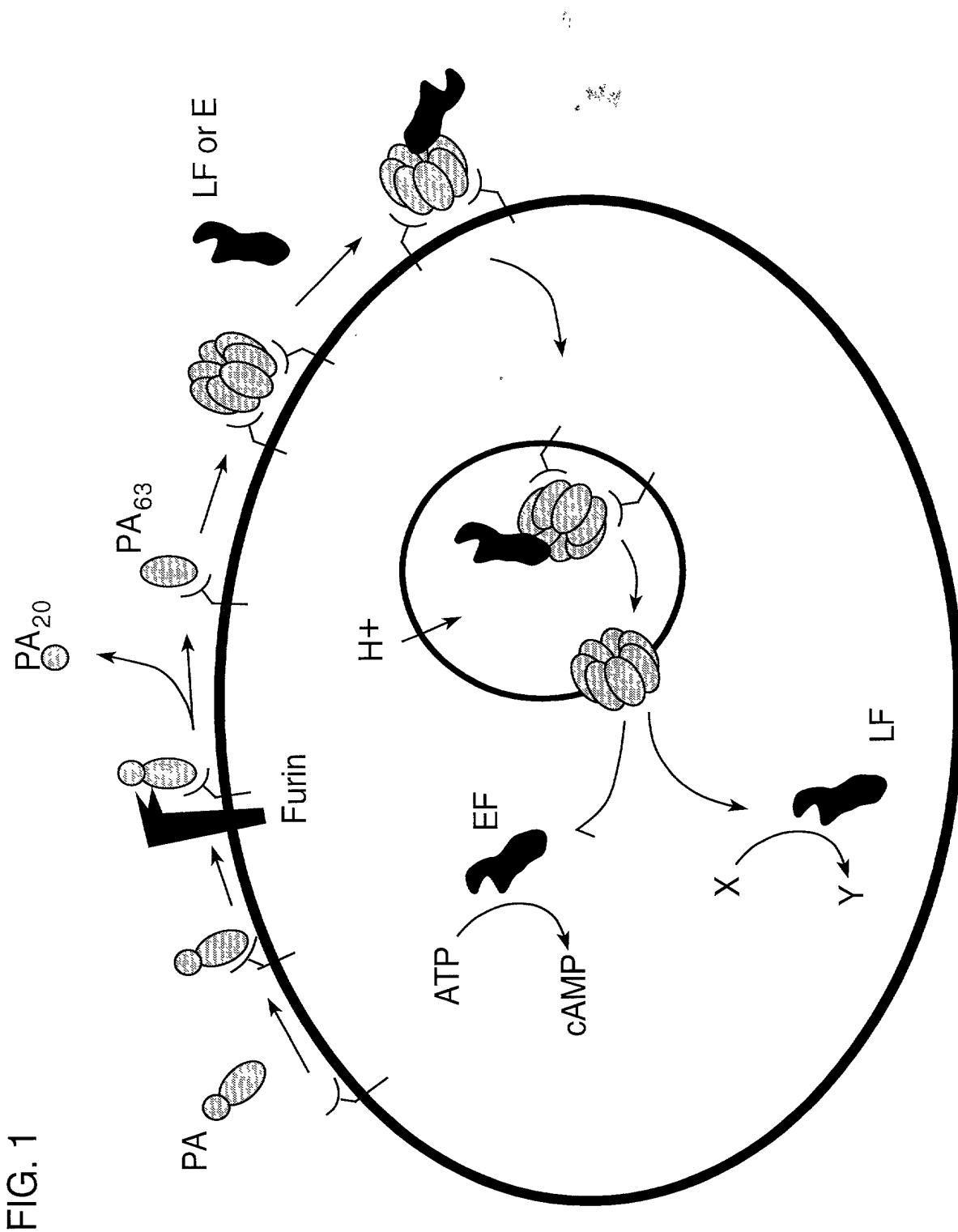
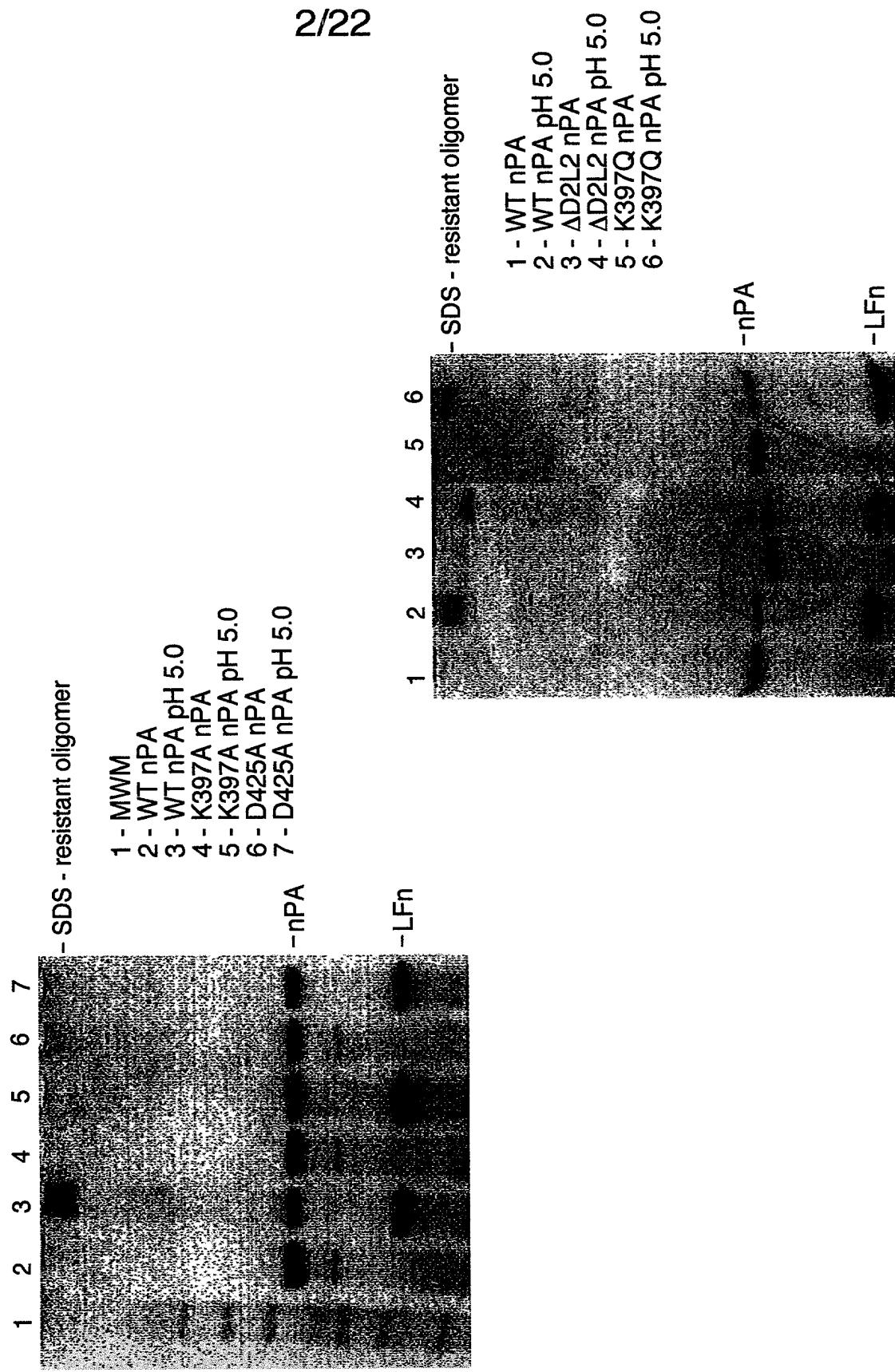


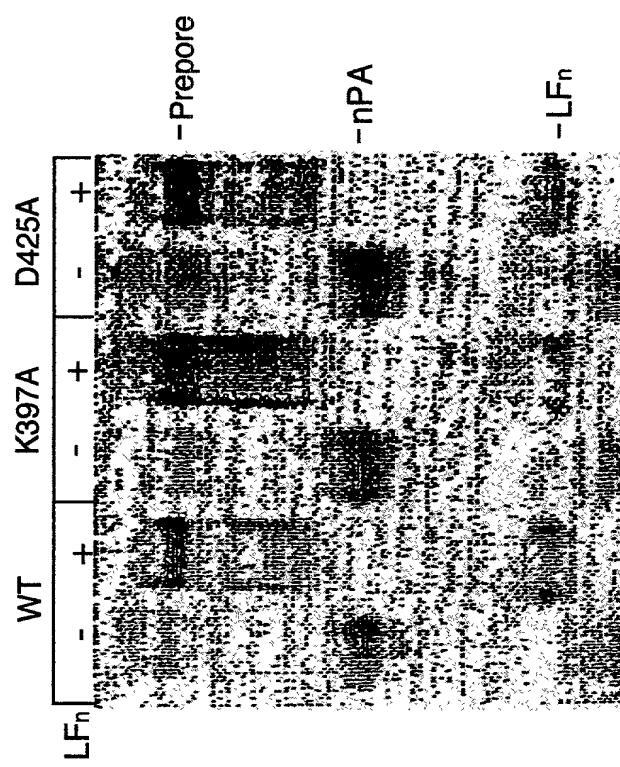
FIG. 1

FIG. 2A



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FIG. 2B



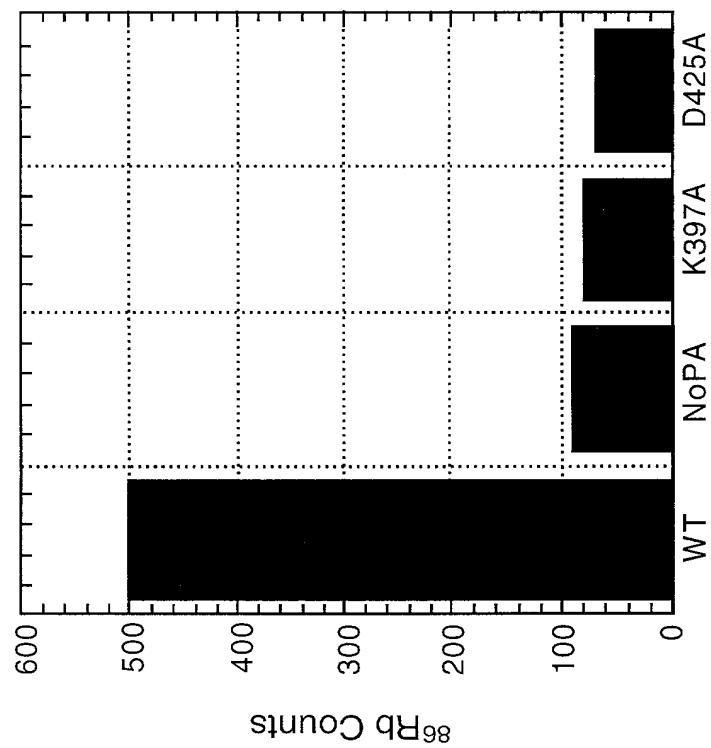


FIG. 3

FIG. 4

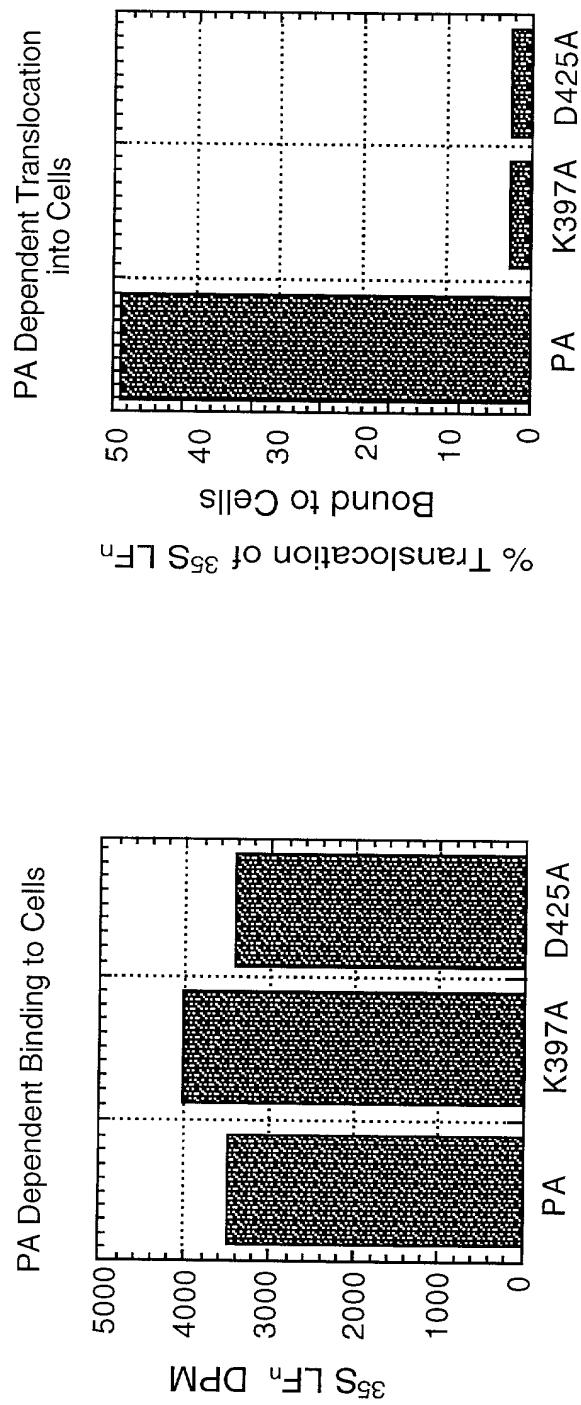


FIG. 5

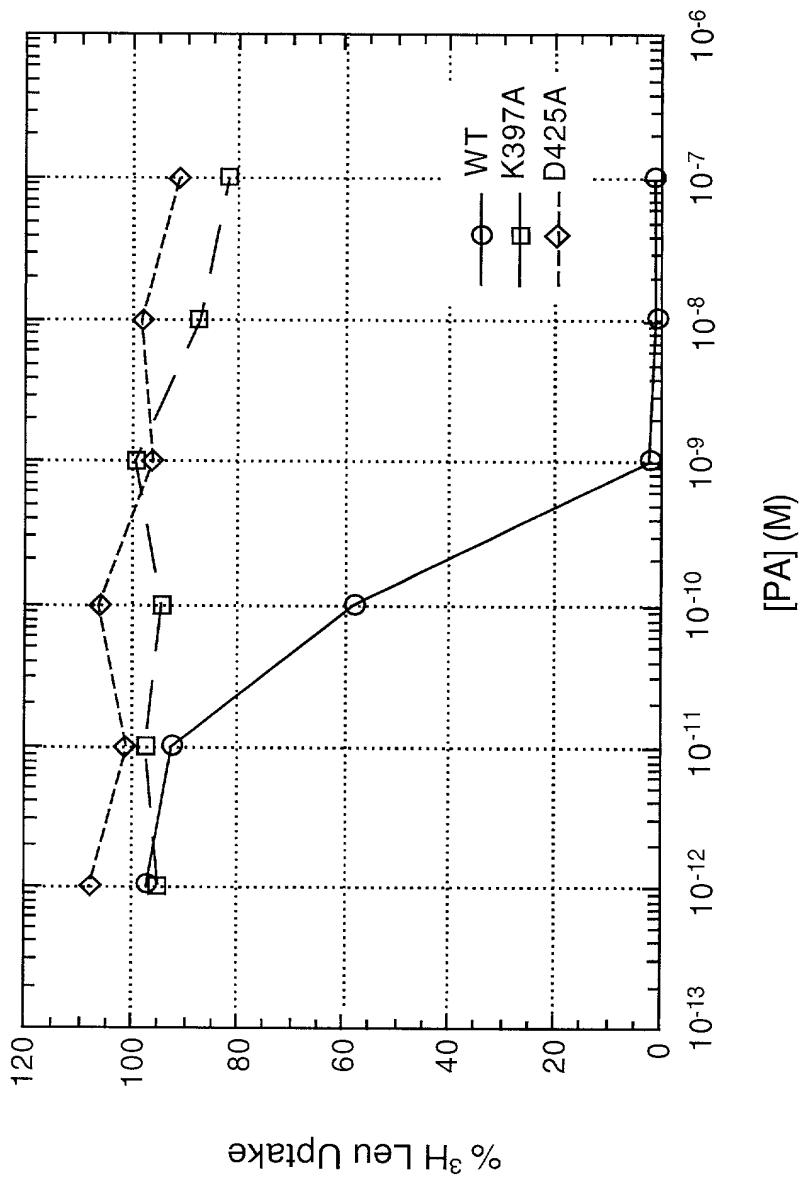
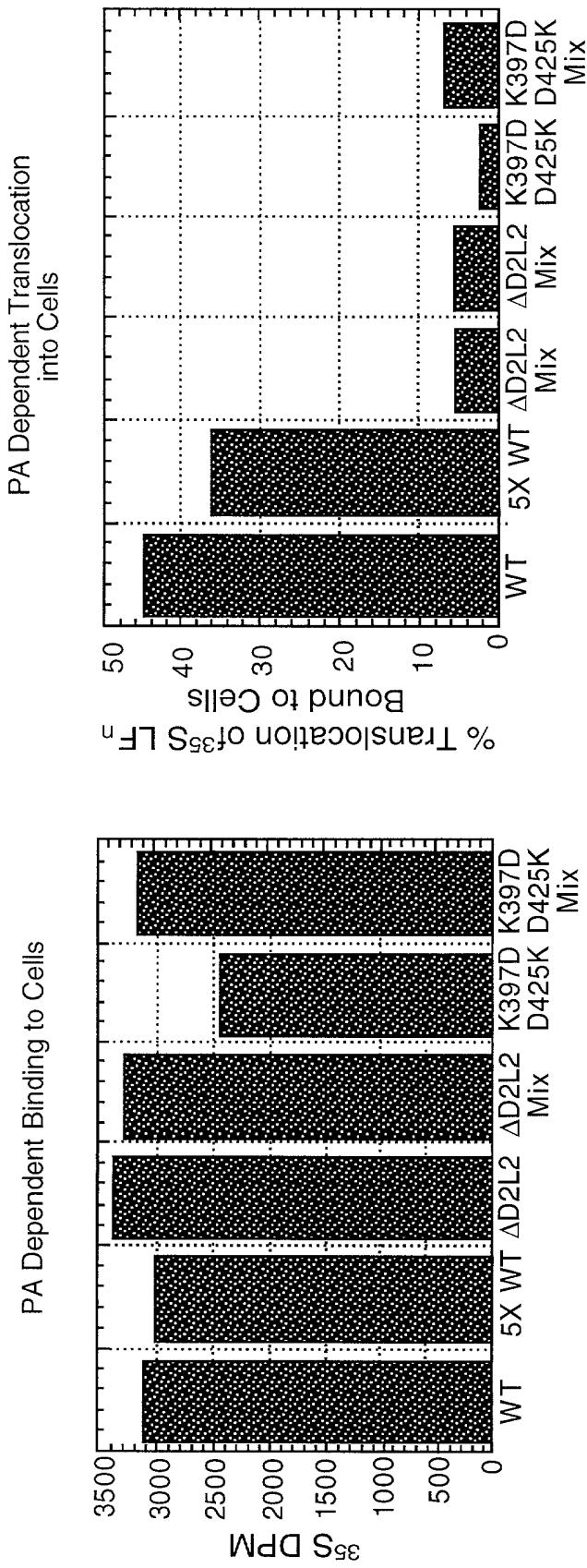
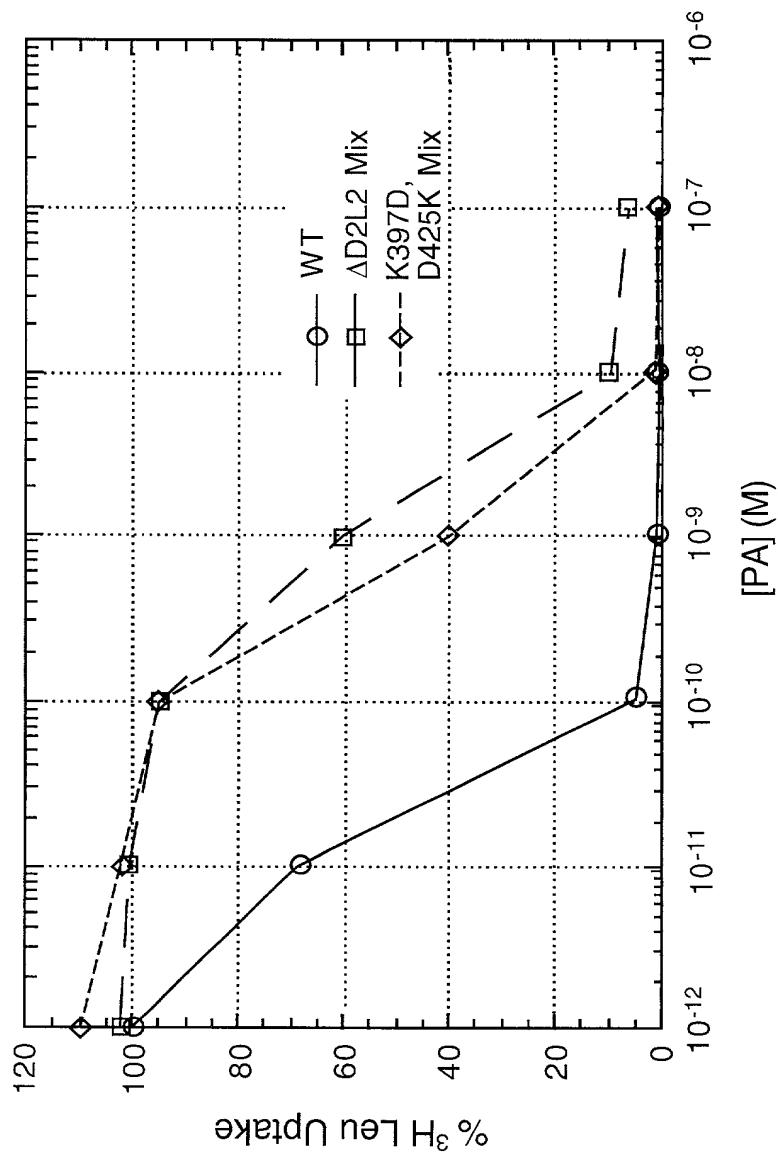


FIG. 6



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FIG. 7



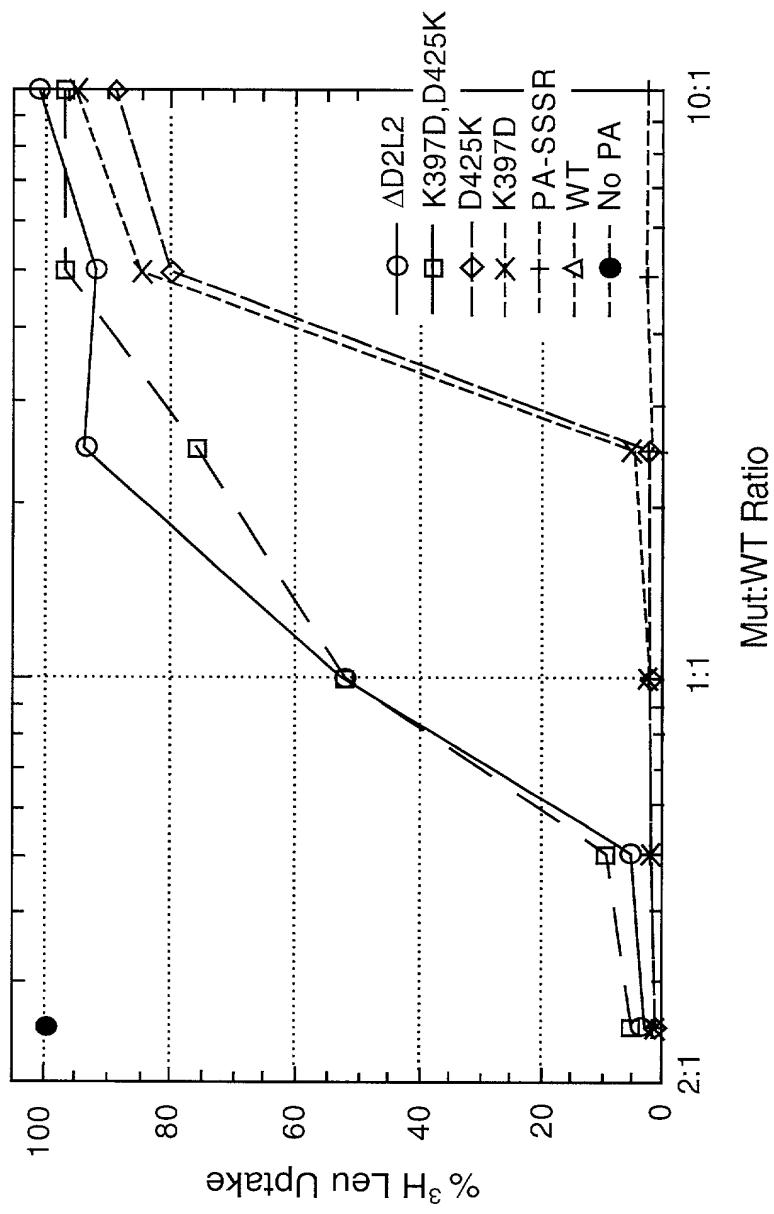
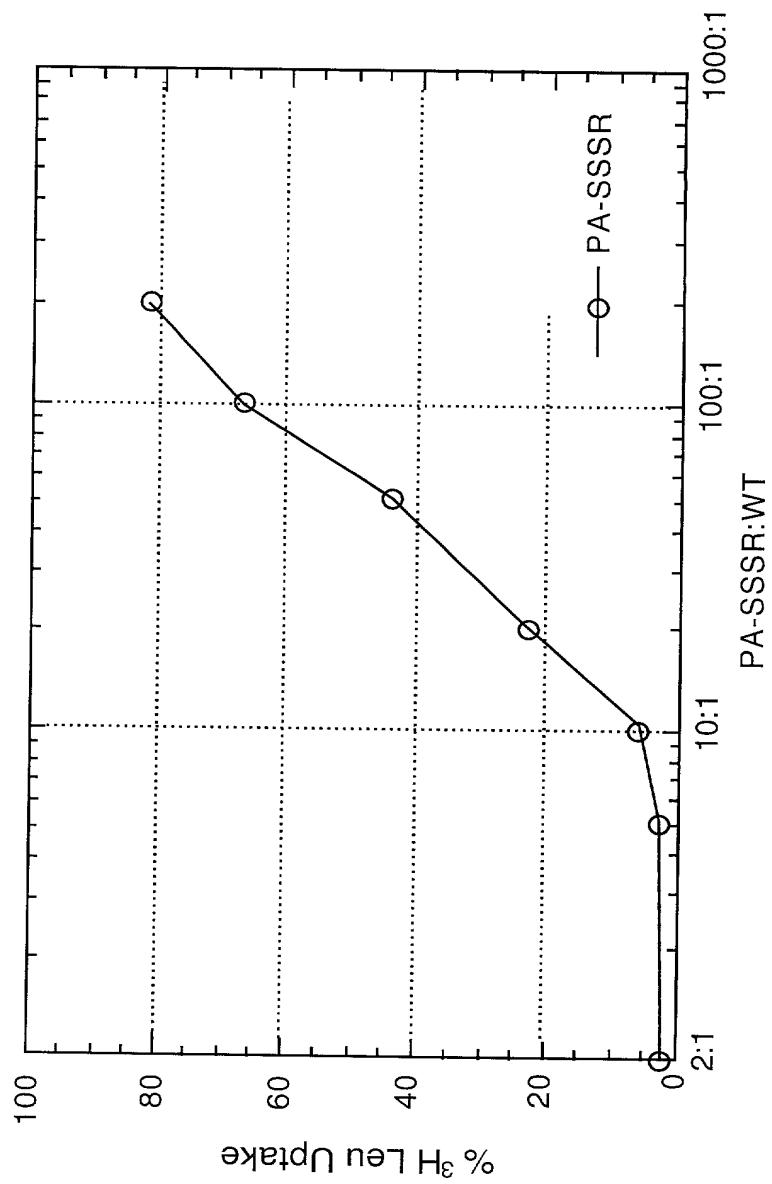


FIG. 8A

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FIG. 8B



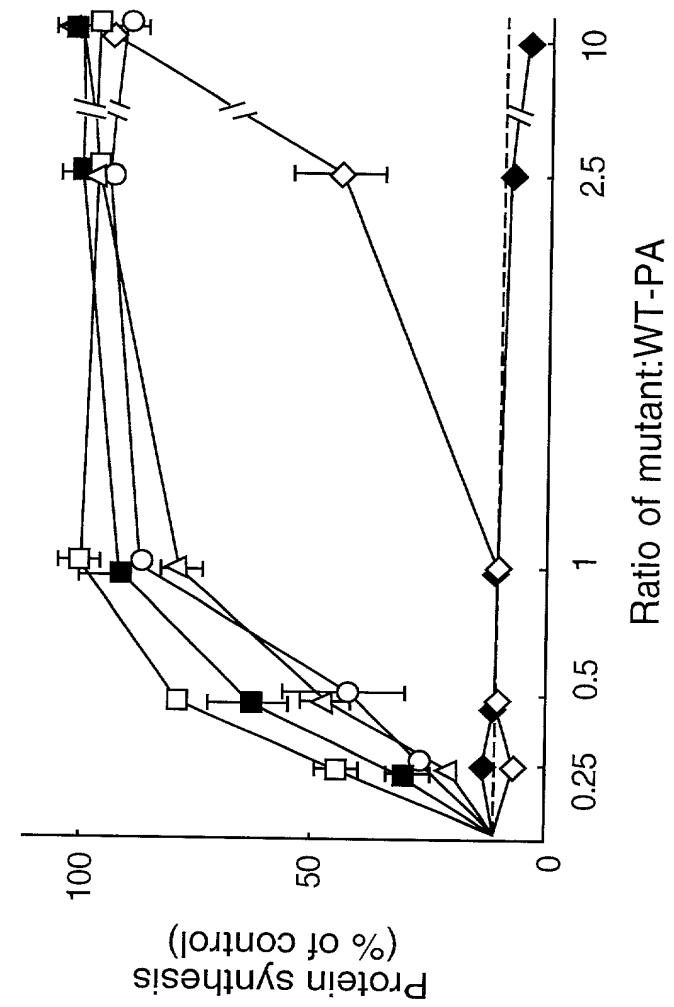


FIG. 9

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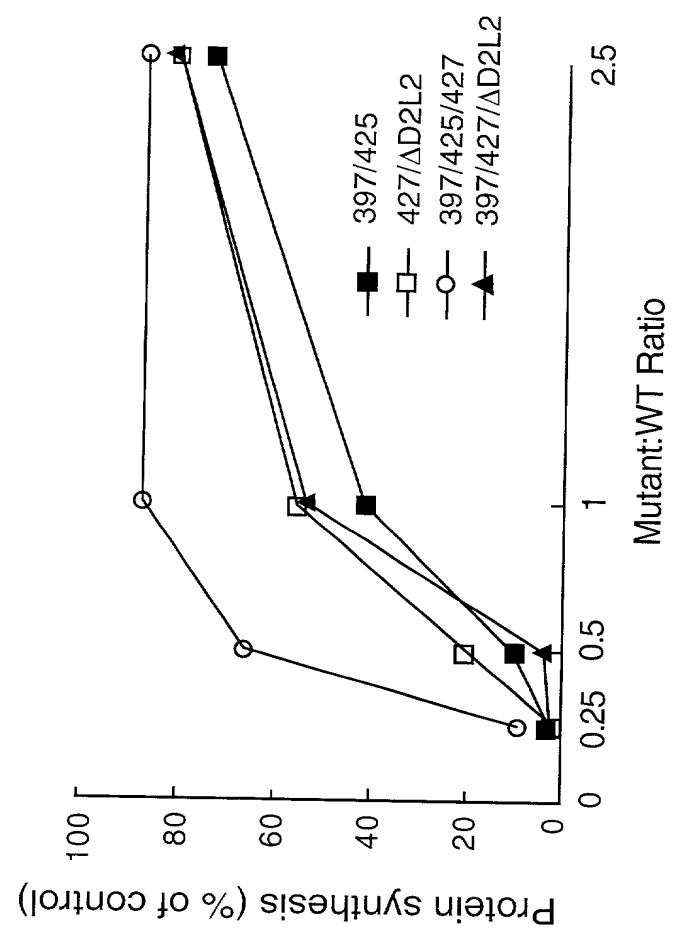


FIG. 10

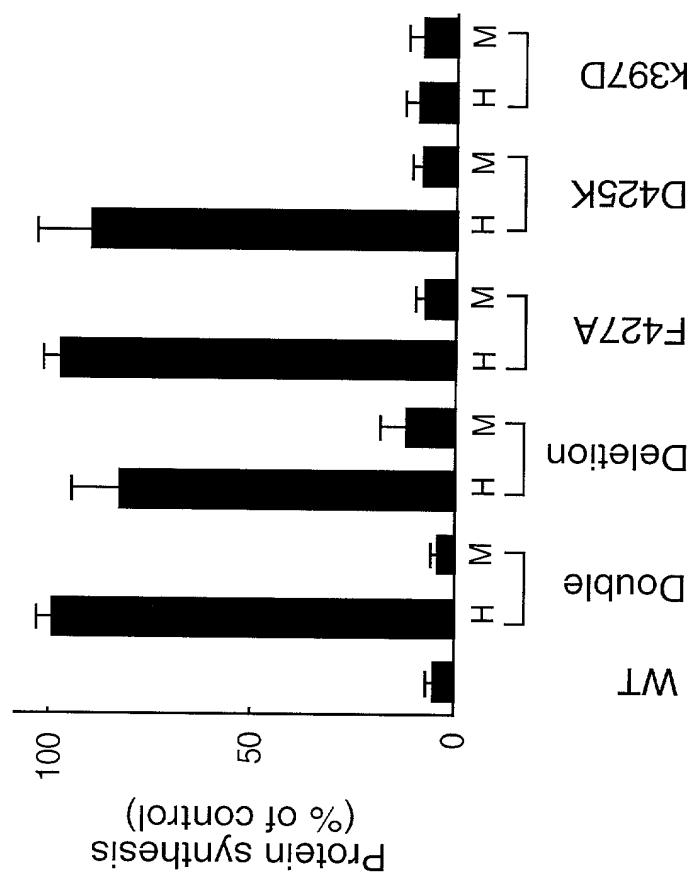


FIG. 11

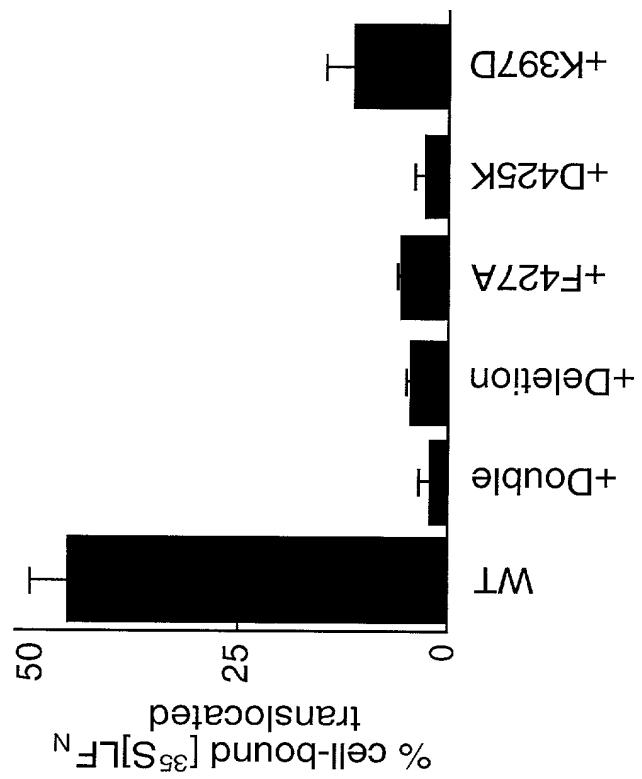


FIG. 12

FIG. 13

Figure 13: SEQ ID No.: 21

EVKQENRLLNESESSSSQGLLGGYFSDLNFQAPMVVTSSSTGDLSSIPSELLENIPSEN
QYFQSAIWSGFIKVKKSDETYTFAT
TSADNHVTMWVDDQEVINAKASNSNKRLEKGRLYQIKIQYORENPTEKGDFKL
YWTDSQNKKVEVISSDNLQLPELKQKS
SNSRKKRSTSAGPTVPDRDNDGPDSLEVEGYTVDVKNKRTFLSPWISNTHEKKG
LTKYKSSPEKWSTASDPYSDFEKVT
GRIDKNVSPEARHPLVAAAYPTVHVDMENILSKNEDQSTQNTDSETRTISKNTSTS
RTHTSEVHGNAEVHASFFDIGSV
SAGFSNSNSSTVAIDHSLSLAGERTWAETMGLINTADTARLNANIRYVNTGTAPIY
NVLPTTSIVLGKNQTLATIKAKENQ
LSQLLAPNNYYPSKKNLAPIALNAQDDFFSSTPITMNYNQFILELEKTKQLRLTDQV
YGNIATYNFENGVRVDTGSNWSEV
LPQIQUETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMLTKEAALKIAFGFNEPN
GNLQYQGKDITEFDFFNFDQQTSQL
NIKNQLAELNATNIYTVDKIKLNAKMINLIRDKRFHYDRNNIAVGADESVVKEA
HREVINSSTEGLLNNDKDIRKILS
GYTVEIEDTEGLKEVINDRYDMNLNISSLRQDGKTFIDFKKYNDKPLYISNPNYKV
NVAVTKENTHINPSENGDTSTNG
IKKLFSSKKGYEIGZ

FIG. 14

Figure 14: SEQ ID No.: 22

GAAGTTAACACAGGAGAACCGGTTATTAAATGAATCAGAATCAAGTCCAGG
GGTTACTAGGATACTATTTAGTGATT
GAATTTCAGCACCCTGGGGTACCTCTACTACAGGGGATTATCTA
TTCCTAGTTCTGAGTTAGAAAATATC
CATCGAAAACCAATATTTCAATCTGCTATTGGTCAGGATTATCAAAGTT
AAGAAGAGTGATGAATATACATTGCT
ACTTCCGCTGATAATCATGTAACAATGTGGTAGATGACCAAGAAGTGATTA
ATAAGCTTCAATTCTAACAAAATCAG
ATTAGAAAAAGGAAGATTATATCAAATAAAAATTCAATATCAACGAGAAAAT
CCTACTGAAAAGGATTGGATTCAAGT
TGTACTGGACCGATTCTCAAAATAAAAAGAAGTGATTCTAGTGATAACTT
ACAATTGCCAGAATTAAAACAAAATCT
TCGAACCTCAAGAAAAAGCGAAGTACAAGTGCTGGACCTACGGTCCAGACC
GTGACAATGATGGAATCCCTGATTCTT
AGAGGTAGAAGGATAACGTTGATGTCAAAAATAAAAGAACCTTTCTTCA
CCATGGATTCTAATATTGAAAGA
AAGGATTAACCAAATATAATCATCTCCTGAAAATGGAGCACGGCTCTGA
TCCGTACAGTGATTGAAAAGGTTACA
GGACGGATTGATAAGAATGTATCACCAGAGGCAAGACACCCCCCTGTGGCAG
CTTATCCGATTGTACATGTAGATATGGA
GAATATTATTCTCTCAAAAATGAGGATCAATCCACACAGAATACTGATAGT
GAAACGAGAACAAATAAGTAAAATACTT
CTACAAGTAGGACACATACTAGTGAAGTACATGGAAATGCAGAAGTGCATGC
GTCGTTCTTGTATTGGGGAGTGT
TCTGCAGGATTAGTAATTGAACTCAAGTACGGTCGCAATTGATCATTCACT
ATCTCTAGCAGGGAAAGAACCTGGC
TGAAACAAATGGGTTAAATACCGCTGATACAGCAAGATTAAATGCCAATATT
AGATATGTAATAACTGGGACGGCTCCAA
TCTACAACGTGTTACCAACGACTTCGTTAGTGTAGGAAAAATCAAACACT
CGCGACAATTAAAGCTAAGGAAAACCAA
TTAAGTCAAATACTTGCACCTAATAATTATTATCCTCTAAAAACTGGCGCC
AATCGCATTAAATGCACAAGACGATT
CAGTTCTACTCCAATTACAATGAATTACAATCAATTCTGAGTTAGAAAAAA
CGAAACAAATTAAAGATTAGATACGGATC
AAGTATATGGGAATATAGCAACATACAATTGAAAATGGAAGAGTGAGGGT
GGATACAGGCTCGAAGTGGAGTGAAGTG
TTACCGCAAATTCAAGAAACAACCGTACATTTAATGGAAAAGATT
AAATCTGGTAGAAAGGCGGATAGCGGC
GGTTAACCTCTAGTGATCCATTAGAAACGACTAAACCGGATATGACATTAAA
GAAGCCCTAAAATAGCATTGGATT
ACGAACCGAATGGAAACTTACAATATCAAGGGAAAGACATAACCGAATTG
ATTAAATTGATCAACAAACATCTCAA
AATATCAAGAATCAGTTAGCGGAATTAAACGCAACTAACATATACTGTAT
TAGATAAAATCAAATTAAATGCAAAAAT

FIG. 14 (CONTINUED)

GAATATTAAATAAGAGATAAACGTTTCATTATGATAAAATAACATAGCA
GTGGGGGGGATGAGTCAGTAGTTAAGG
AGGCTCATAGAGAAGTAATTAAATTCGTCAAACAGAGGGATTATTGTTAAATAT
TGATAAAGGATAATAAGAAAAATAATTATCA
GGTTATATTGTAGAAATTGAAGATACTGAAGGGCTTAAGAGAAGTATAAATG
ACAGATAAGATAATTCTAG
TTACGGCAAGATGGAAAACATTATAAGTTAAAATAATGATAAAA
TTACCGTTATATAAGTAATCCCAATT
ATAAGGTAATGTATATGCTGTACTAAAGAAAACACTAATTATAATCCTAGT
GAGAATGGGGATACTAGTACCAACGGG
ATCAAGAAAATTAAATCTTTCTAAAGGCTATGAGATAGGATAAA

FIG. 15

FIG. 15 (CONTINUED)

FIG. 16

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PA

| | |
|---------|---|
| PA | |
| cdADPRT | |
| cpiots | |
| csirts | |
| cbs2 | |
| VIP1 | MIRMEGK LPMVSIKKLQVVVINTVLLSTVPSISSLNNEVILAEQLNINQS SKYDNLQLKITEKVVEPKEDK |

PA

| | |
|---------|--|
| PA | |
| cdADPRT | |
| cpiots | |
| csirts | |
| cbs2 | |
| VIP1 | EKAKEW GKEKEKEW KLTATELGKMMHIFLDDKNDIATKTYKEITE SLAGSFEDIEKDLKEIDKMDPKTILSII |

PA

| | |
|---------|---|
| PA | |
| cdADPRT | |
| cpiots | |
| csirts | |
| cbs2 | |
| VIP1 | SIIIIYKIVVEFTTIGFNIKSLTEGNTIMS DAKAQFKEQFLDRDIKFDSYLDTHLTAAQVSSKE RVIK VIVF |

PA

| | |
|---------|--|
| PA | |
| cdADPRT | |
| cpiots | |
| csirts | |
| cbs2 | |
| VIP1 | SGKGSTTPTKAGVILHNSETKLLIDNGYKVHVDRVSKVVKNGVZCLQI EGT LKNSLD FKHD INRAAHSWG |

PA

| | |
|---------|---|
| PA | |
| cdADPRT | |
| cpiots | |
| csirts | |
| cbs2 | |
| VIP1 | MKNTTEEWAKDLTDQREALIGYARQDLYKEIINIVLRNQGGSGHEKLDQIKNISDALGKKFIPENITVYRM |

PA

| | |
|---------|--|
| PA | |
| cdADPRT | |
| cpiots | |
| csirts | |
| cbs2 | |
| VIP1 | CGMFEPFGYQISLFPLSLKDPHEQFLNITIKE DKGYKSTSLSSEERLAAPGSRKTLRLQVPRGSGTGY LSAT |

PA

| | |
|---------|---|
| PA | |
| cdADPRT | |
| cpiots | |
| csirts | |
| cbs2 | |
| VIP1 | MKIQMRRNNKXVLSLT LTAKVSQALVIFPVIAQTSTSNS MKIQIINIVSELT LTAMISQTLSVIVVIAQTITOND MKDNKKE LGLLTCTVLVGQKMTYFVYIAQTITOND MLVSIF GGPASEKNEILLDLSKYHIDEVIEVINGVKRYVVVATL LTNISRGFSTFFTFSFTFFFSDIGSTMKTII |

β_1 β_2 η_1 η_2 β_3
 PA TT 40 50 60 70
 10 20 30 40 50 60
 VIQEPDRLNEssS S C G I G Y P S D L N P Q A F H V V T S I S T S P s I P S S I D E M I F S Z
 S I I I I I V N E I I F R N N G M G V I P S L E H P R L I N I K A F I K I K I D P E E K V U K I L L D K S U V R S I R M T G R I I
 T M O R E I T H E I T L S I N G M G V I P S L E H P R L I N I K A F I K I K I D P E E K V U K I L L D K S U V R S I R M T G R I I
 D N Q E I T T H E I T V S S N G M G V I P S L E H P R L I N I K A F I K I K I D P E E K V U K I L L D K S U V R S I R M T G R I I
 E H I S M Q S I N R D I P T I N G M G V I P S L E H P R L I N I K A F I K I K I D P E E K V U K I L L D K S U V R S I R M T G R I I
 G R S I T T O R M O O K E M I K R G L I G T P R G K D P S I L T P D P F R D S H I T M Q O T A P I K I L L K K O D E Y S I R M I G L D C

β_4 η_3 β_5 β_6 β_7 β_8 β_9
 PA AAA TT 100 110 120 130
 80 90 100 110 120 130
 VRRISLEYTFATsAIIHIVVWVDDOEVINIAASpIPIRKLIPsRGRILYTRIQM F P B K C D P R Y M
 cdADPRT F S R K I G E Y T I L S T P R K . . . V I K Q M . . . T E S T I S H T I L K V D K M K R E Y V R E I E Q . . . D R H I L G S I D P I I S F R Y M
 cpiots F S E N I G E Y T I L S T P R K . . . V I K Q M . . . A K G D I A P T L K V D K M K R E Y V R E I E Q . . . D R H I L G S I D P I I S F R Y M
 csirts F S R K I G E Y T I L S T P R K . . . V I K Q M . . . A E G I A P T L K V D K M K R E Y V R E I E Q . . . D R H I L G S I D P I I S F R Y M
 cbs2 F S I T G E Y T I L S T P R K . . . V I K Q M . . . D S E N O I L K A N I E G I R Y M . . . D S E N O I L K A N I E G I R Y M
 VIP1 S K E T G F E T E M I S E D Q A I I E L H G K I I S H K G K E R K O V V H E R G I Y P E R I E Q . . . D T P R I I S K T E P L K E F

FIG. 16 (CONTINUED) 21/22

| | |
|---|---|
| PA cdADPRT cpiota ciota cbz2 VIP1 | <p>Diagram illustrating sequence alignment of PA, cdADPRT, cpiota, ciota, cbz2, and VIP1 across various regions (beta 10 to beta 38). The diagram shows the relative positions of amino acids and the presence of gaps in the sequences.</p> <p>Regions:</p> <ul style="list-style-type: none"> Region 1 (Beta 10 to Beta 11): PA (140-150), cdADPRT (140-150), cpiota (140-150), ciota (140-150), cbz2 (140-150), VIP1 (140-150). Region 2 (Beta 12 to Beta 13): PA (160-170), cdADPRT (160-170), cpiota (160-170), ciota (160-170), cbz2 (160-170), VIP1 (160-170). Region 3 (Beta 14 to Beta 15): PA (200-210), cdADPRT (200-210), cpiota (200-210), ciota (200-210), cbz2 (200-210), VIP1 (200-210). Region 4 (Beta 16 to Beta 17): PA (270-280), cdADPRT (270-280), cpiota (270-280), ciota (270-280), cbz2 (270-280), VIP1 (270-280). Region 5 (Beta 18 to Beta 19): PA (330-340), cdADPRT (330-340), cpiota (330-340), ciota (330-340), cbz2 (330-340), VIP1 (330-340). Region 6 (Beta 20 to Beta 21): PA (400-410), cdADPRT (400-410), cpiota (400-410), ciota (400-410), cbz2 (400-410), VIP1 (400-410). Region 7 (Beta 22 to Beta 23): PA (440-450), cdADPRT (440-450), cpiota (440-450), ciota (440-450), cbz2 (440-450), VIP1 (440-450). Region 8 (Beta 24 to Beta 25): PA (470-480), cdADPRT (470-480), cpiota (470-480), ciota (470-480), cbz2 (470-480), VIP1 (470-480). Region 9 (Beta 26 to Beta 27): PA (500-510), cdADPRT (500-510), cpiota (500-510), ciota (500-510), cbz2 (500-510), VIP1 (500-510). Region 10 (Beta 28 to Beta 29): PA (540-550), cdADPRT (540-550), cpiota (540-550), ciota (540-550), cbz2 (540-550), VIP1 (540-550). Region 11 (Beta 30 to Beta 31): PA (560-570), cdADPRT (560-570), cpiota (560-570), ciota (560-570), cbz2 (560-570), VIP1 (560-570). Region 12 (Beta 32 to Beta 33): PA (600-610), cdADPRT (600-610), cpiota (600-610), ciota (600-610), cbz2 (600-610), VIP1 (600-610). Region 13 (Beta 34 to Beta 35): PA (620-630), cdADPRT (620-630), cpiota (620-630), ciota (620-630), cbz2 (620-630), VIP1 (620-630). Region 14 (Beta 36 to Beta 37): PA (640-650), cdADPRT (640-650), cpiota (640-650), ciota (640-650), cbz2 (640-650), VIP1 (640-650). Region 15 (Beta 38 to Beta 39): PA (670-680), cdADPRT (670-680), cpiota (670-680), ciota (670-680), cbz2 (670-680), VIP1 (670-680). |
|---|---|

FIG. 16 (CONTINUED)

PA TT - - - - - 698 709 719 729 TT
 PA **PA** T H D K L F L V I S P H Y K V R U V A V I R E P T I X H F S E N G D I S T I N G .
 cdADPRT D A H K I Y F A D L H E D P S T G H T Y I N G M Y F A P T Q T H K B A L D Y I Q K Y R V E A T L Q Y S G P R D I G T K D K E M R J V L G D F
 cpiots D A H K I Y Y A D I K L D I N G T H Y I L G Y F E P T Q T H K B A L D Y I Q K Y R V E A T L Q Y S G P R D I G T K D K E M R J V L G D F
 csiots D A H K I Y Y A D L S F H Q S T A H Y Y L G Y F E P T Q T H K B A L D Y I Q K Y R V E A T L Q Y S G P R D I G T K D K E M R J V L G D F
 abc2 D L P H Y I L Y S S P D K G Y Y D E P P Y P Y I N G S R S P E N I S C D I I N S E R .
 VIP1 S R V G I K L E D G I L I D K G G I H Y G E F I N E A S P H E F L Q N Y V I T R Y E V T Y S S E L G P D M A T L E S D K R I Y K D G T K